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Run on:

Sequence:

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Database

Result No.

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Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist; therapy; diagnosis; ss.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                               A DNA sequence (AAT17869) coding for human interleukin-11 (IL-11) receptor alpha chain (AAR92814) is a composite of 4 cDNA clones isolated from a bone marrow library using a murine IL-11 receptor alpha chain cDNA (see AAT17868) fragment as probe. The sequence can be inserted into a vector and used for prodn. of IL-11 receptor, useful for developing therapeutic (ant)agonists or in diagnosis.
                                                                                                                                                                                                                                                        TCTAACAGCCTTACCCCACTTGGTGCATCTATTTTTCTCCTAGGAAGCCTCAGTTTTGGA
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                                     Nucleic acid encoding haemopoietin receptor amino acid motif esp. IL-11 receptor alpha cdeveloping IL-11 (ant)agonists
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iive 0; Mismatches
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                                                                                                       IL-11 receptor; antibody; antagonist;
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Pred. No. 0;
0; Mismatches
                                                                                                                  Paget disease; myeloma; ds
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/*tag= b
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                                                                                 Human interleukin-11 receptor cDNA.
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99.0%;
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Best Local Similarity
                     standard;
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                                                                                                                 osteoporosis;
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786 ccctggtgtctgcctccccctgcccccaggcctggggcccccaggggtccagtatg
                                       GGCAGCCAGGCAGGTCCGTGAAGCTGTGTCCTGGAGTGACTGCCGGGGGACCCAGTGT
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WPI; 2000-679539/66

Nyce JW;

Thu Oct

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Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pain; cystic fibrosis; allergic rhinitis; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                              2222
              tectgggaetggtggetggggeeetggeactgggetetggetgaggetgagaegggggtg 1922
                                                         GTCTTGCTGGTGTG------GATAGAAACCAGGCAGGACAGTAGATCCCTATGG 1487
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                                                                                                                                                                                                                                                                                                                         Human low adenosine antisense oligonucleotide related sequence #2525.
                                                                                                CAGGAGCTCCAAACCTGTAGAGGACCCAGGAGGCCTTCGGCAGATTCCACCTATAATCCT
                                                                                                                2223 aacgigigiaaigigiacatcigigiccaigigaccaigigicigigicaggaac
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TGGCCTTTCCCCTTGCAGGGTTGTGCAGGTGTGAATAAAGAGAATAAAGGAAGTTCTTGG
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J W.
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The present invention userinces tow demonstrate (n) content and teanses oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base.

(I) can have respiratory, bronchodilator, antiinflammatory, analgealc, immunosuppressive, antisathmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activity of target polypeptides associated with lung/respiratory disorders and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokine and chemokine receptors and antibodies, antibody receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system creceptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system creceptors, brading proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary distress syndrome and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasconstruction, allergy (ist) and/or surfactant hypoproduction which are associated with a disease (CNS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary transplantation rejection, pulmonary infections, bronchitis, pulmonary transplantation rejection, pulmonary infections, bronchitis, and antisense oligonucleotides used in the exemplification of fragments and antisense oligonucleotides used in the exemplification of the present invention.
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                                                                                                       Low adenosine (A) content antisense oligonucleotides which do not
trigger adenosine receptors during metabolism, useful e.g. for treating
cancers and respiratory obstructions -
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                                                                                                                                                                                                                                            present invention describes low adenosine (A) content antisense
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.0%; Score 1638.6;
llarity 99.5%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                 Disclosure; Page 762; 1592pp; English
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The present invention describes low adenosine (A) content antisense oligonuclectides and compositions (I) comprising them. In the antisense cligonuclectides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonuclectides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system
                                                                                                                                                                                                                                                                                                                                                                                                          Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
                                                                        1745
                                                                                                         1618
                                                                                                                                                                                                                                                                                                                                                                            Human low adenosine antisense oligonucleotide related sequence #2887
 1686 TGTATGTAGGTGCCTGGGGAGTGTGTGTGGGTCCTTGGCTCTTGGCCTTTCCCCTTGCAG
                                                                                        Disclosure; Page 1324-1325; 1592pp; English
                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                     standard; DNA; 1682
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(NYCE/) NYCE
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receptors, CNS and peripheral nervous and non-nervous system peptide transmitters. defensins, growth factors, vascactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease condition selected from pulmonary vascoconstriction, inflammation, allergyies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary transplantation rejection, pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAR18434 to AAR21843 represent human polynucleotide the processing the exemplification of the present invention. 

Sequence 1682 BP; 324 A; 476 C; 521 G; 361 T; 0 other;

2 AGATGAGCAGCAGCTGCTCAGGGCTGAGCAGGTCCTGGTGGCCGTGGCTACAGCCCTGG 185 245 305 183 365 425 303 485 545 423 483 665 725 603 785 099 845 720 905 tgtctgcctcctccccctgccccaggcctggggcccccagggggtccagtatgggcagc 123 63 Gaps TTCGGGATGGGGAGCCAAAGCTGCTCCAGGGACCTGACTCTGGGCTAGGGCATGAACTGG TCCTGGCCCAGGCAGACAGCACTGATGAGGGCACCTACATCTGCCAGACCCTGGATGGTG gtgttgtccacggggctgagttctggagccagtaccggattaatgtgactgaggtgaacc agatgagcagctgctcaggggctgagcagggtcctggtggccgtggctacagccctgg TGTCTGCCTCCTCCCCTGCCCCAGGCCTGGGGCCCCCCCAGGGGTCCAGTATGGGCAGC CAGGCAGGTCCGTGAAGCTGTGTTGTCCTGGAGTGACTGCCGGGGACCCAGTGTCCTGGT ttcgggatggggagccaaagctgctccagggacctgactctgggctagggcatgaactgg TACCCACCCGCTACCTCCTACAGGAAGAAGACAGTCCTAGGAGCTGATAGCCAGA GGAGGAGTCCATCCACAGGGCCCTGGCCATGCCCACAGGATCCCCTAGGGGCTGCCCGCT GTGTTGTCCACGGGGCTGAGTTCTGGAGCCAGTACCGGATTAATGTGACTGAGGTGAACC CACTGGGTGGTGCCAGCACACGCCTGCTGGATGTGAGCCTTGCAGAGCATCTTGCGCCCTG cactg---ggtgccagcacacgcctgctggatgtgagcttgcagagcatcttgcgccctg ACCCACCCCAGGGCCTGCGGGTAGAGTCAGTACCAGGTTACCCCCGAGGCCTGCGAGCCA GCTGGACATACCCTGCCTCCTGGCCGTGCCAGCCCCCACTTCCTGCTCAAGTTCCGTTTGC 21; Length 1682; 5; 4; Indels DB Score 1638.6; Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 99.5%;
Matches 1666; Conservative 126 4 186 64 246 124 306 184 366 244 426 304 186 364 546 124 909 484 999 544 726 604 984 661 846 ð g g ò q ò q ò q ò g ò g ò g ò g ò D. ò ď ò g Ω

1140 TGTACCTCTGATTTCACCCCAGAGTTGGAGTTCTGCTCAAGGAACGTGTGTAATGTGTAC 1625 ctggtgtggatagaaaccaggcaggacagtagatccctatggttggatctcagctggaag 1380 TGTATGTAGGTGCCTGGGGAGTGTGTGTGGGTCCTTGGCTCTTGGCCTTTCCCCTTGCAG 1745 aggingacagocotgotocotocaaggocotocotocaacoacacotoggotactigato 1080 atggatccccaaagcctgggttcttggcctcagtgattccagtggacaggcgtccaggag 1260 gotggacataccetgcctcctggccgtgccagccccacttcctgctcaagttccgtttgc 780 AGTACCGTCCGGCGCAGCATCCAGCCTGGTCCACGGTGGAGCCAGCTGGACTGGAGGAGG TAGATGCTGGCACCTGGAGCACCTGGAGCCCGGAGGCCTGGGGAACTCCGAGCACTGGGA tagatgctggcacctggagcacctggagcccggaggcctggggaactccgagcactgggga CCATACCAAAGGAGATACCAGCATGGGGCCAGCTACACACGCAGCCAGGCGGGGGGCCTC AGGTGGACAGCCCTGCTCCTCCAAGGCCCTCCCTCCAACCACACCCTCGGCTACTTGATC ACAGGGACTCTGTGGAGCAGGTAGCTGTGCTGGCGTCTTTGGGAATCCTTTCCTGG GACTGGTGGCTGGGGCCCTGGCACTGGGGCTTTGAGCTTGAGACGGGGTGGGAAGG ATGGATCCCCAAAGCCTGGGTTCTTGGCCTCAGTGATTCCAGTGGACAGGCGTCCAGGAG CTCCAAACCTGTAGAGGACCCAGGAGGGCTTCGGCAGATTCCACCTATAATCCTGTCTTG CTGGTGTGGATAGAAACCAGGCAGGACAGTAGATCCCTATGGTTGGATCTCAGCTGGAAG TTCTGTTTGGAGCCCATTTCTGTGAGACCCTGTATTTCAAATTTGCAGCTGAAAGGTGCT TGATCACAGATGCTGTGGCTGGCTGCCCCATGCTGTACGAGTCAGTGCCGGGACTTTC GGGTTGTGCAGGTGTGAATAAAGAGAATAAGGAAGTTCTTGGAGATTATACTCAG 1800 NO:2525 G polynucleotide SEQ Human adenosine receptor related BP. 1682 (first entry) DNA; AAA34836 standard; 28-JUL-2000 AAA34836; 841 901 1086 1021 1206 1081 1141 1201 1386 1261 1446 1321 1506 1381 1441 1501 1686 1561 1619 1026 1266 1326 1566 1626 906 781 996 961 1146 1746 AAA34836
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antisense oligonaclectide (NON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory antialergies, and/or inflammation. The ON can have antiinflammatory antialergies, and/or antiaathmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impediated airways, including lung disease and diseases secondary effects affilict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, astham, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metestasise to the lungs, including carcinomas, and cancers which may metastasise to the lungs, including the ONS reduces side effects. The A-containing ONS break down with the relass of deoxyadenosine which activates adenosine receptors causing ronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present of invention, which crorrespond to SEQ ID NO: 1 to 2815, and then the last 185 sequences are also called SEQ ID NO: 1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO: 1 to 185, untile present invention do not match up with their corresponding SEQ ID NO: sequences given in the disclosure of the present invention and including to release of the present invention do not match up with their corresponding SEQ ID NO: sequences phosphorothioate; impaired respiration; infllammation; allergy; allergy; allergy; antiasted disease; bronchoconstration; inhibitor; antianflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss. adenosine receptor; low adenosine antisense oligonucleotide; New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or present invention describes a new composition comprising an Disclosure; Page 691-692; 1343pp; English. 98US-0095212. 99WO-US17712 EAST CAROLINA WPI; 2000-205971/18. WO200009525-A2. (UYEC-) UNIV 03-AUG-1998; 03-AUG-1999; 24 - FEB - 2000 Nyce JW; cancers Ношо 

Sequence 1682 BP; 324 A; 476 C; 521 G; 361 T; 0 other;

5 TGTCTGCCTCCTCCCCCTGCCCCCAGGCCTGGGGCCCCCCAGGGGTCCAGTATGGGCAGC 245 126 AGATGAGCAGCAGCTGCTCAGGGCTGAGCAGGGTCCTGGTGGCCGTGGCTACAGCCCTGG 185 5; Gaps Score 1638.6; DB 21; Length 1682; 4; Indels Pred. No. 0; 0; Mismatches 91.0%; 99.5%; Best Local Similarity 99.5 Matches 1666; Conservative Query Match 4 981 64 ò 셤 δ a

1025 1085 1145 1326 ATGGATCCCCAAAGCCTGGGTTCTTGGCCTCAGTGATTCCAGTGGACAGGCGTCCAGGAG 1385 900 096 905 780 965 840 543 725 785 099 845 720 183 425 485 363 423 605 483 665 603 GTGTTGTCCACGGGCTGAGTTCTGGAGCCAGTACCGGATTAATGTGACTGAGGTGAACC 901 tagatgctggcacctggagcacctggagcccggaggcctggggaactccgagcactggga 1086 CCATACCAAAGGAGATACCAGCATGGGGCCAGCTACACACGCAGCCAGAGGTGGAGCCTC 1146 AGGTGGACAGCCCTGCTCCTCCAAGGCCCTCCCAACCACACCTCGGCTACTTGATC 364 gccaagcagccgactatgagaacttctcttgcacttggagtcccaggccagatcagcggtt 484 ggaggagtccatccacagggccctggccatgcccacaggatcccttaggggctgccgct 726 CACTGGGTGGTGCCAGCACACGCCTGCTGGATGTGAGCTTGCAGAGCATCTTGCGCCCTG 786 ACCCACCCCAGGGCCTGCGGGTAGAGTCAGTACCAGGTTACCCCCGAGGCCTGCGAGCCA GCTGGACATACCCTGCCTCCTGGCCGTGCCAGCCCCACTTCCTGCTCAAGTTCCGTTTGC AGTACCGTCCGGCGCAGCATCCAGCCTGGTCCACGGTGGAGCCCAGCTGGACTGGAGGAGG TGATCACAGATGCTGTGGCTGGCTGCCCCATGCTGTACGAGTCAGTGCCCGGGACTTTC 1026 TAGATGCTGGCACCTGGAGCACCTGGAGCCCGGAGGCCTGGGGAACTCCGAGCACTGGGA 1206 ACAGGGACTCTGTGGAGCAGGTAGCTGTGCTGGCGTCTTTGGGAATCCTTTCCTGG GACTGGTGGCTGGGGCCCTGGCACTGGGGCTCTGGCTGAGGCTGAGACGGGGTGGGAAGG gactggtggctggggccctggcactggggctctggctgaggctgagacggggtgggaagg TTCGGGATGGGGAGCCAAAGCTGCTCCAGGGACCTGACTCTGGGCTAGGGCATGAACTGG TCCTGGCCCAGGCAGACAGCACTGATGAGGGCACCTACATCTGCCAGACCCTGGATGGTG 304 cacttggggggacagtgaccetgcagetgggctaccetccagcccgccetgttgtctcct TACCCACCCGCTACCTCACCTCCTACAGGAAGAAGACAGTCCTAGGAGCTGATAGCCAGA CAGGCAGGTCCGTGAAGCTGTTGTCCTGGAGTGACTGCCGGGGACCCAGTGTCCTGGT GGAGGAGTCCATCCACAGGGCCCTGGCCATGCCCCACAGGATCCCCTAGGGGGTGCCCGCT 961 1081 906 966 846 246 306 184 366 426 486 909 g g Op δy g Qγ g g g g ŏ qq g ò g δ δ δ g ò g δ g à Db qq 셤 q δy ŏ ò ò ò Q δy ŏ

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Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergy; allergic disease; bronchoconstriction; inhibitor; antiniflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
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           atggatccccaaagcctgggttcttggcctcagtgattccagtggacaggcgtccaggag 1260
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                                                                                                                                                                                                                                                             New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
CTCCAAACCTGTAGAGGACCCAGGAGGGCTTCGGCAGATTCCACCTATAATCCTGTCTTG
                                                                                                                                                                                                                                                                                                                                                                       1746 GGGTTGTGCAGGTGTGAATAAAGAGAATAAGGAAGTTCTTGGAGATTATACTCAG 1800
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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, cartiages nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, cartiarys, including lung disease activities. The compositions are useful for the treatment of diseases associated with inflammation, impeded respiration, respiratory distease whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distease storing pain, cystic pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, asthma, impeded respiration, respiratory distease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONS reduces side effects. The A-containing ONS break down with the relates of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA33313 to AAA33312 represent the nucleotide sequences given in the sequence listing from the present (AAA3323 to AAA3332) are specifically claimed ONS from the present invention. Whis Sequences Sequences SEQ ID NO: sequences in the sequence of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence of the present invention and the present invention and sequence instruction and sequences are also called sequences. SEQ ID NO: sequences given in the sequence of the present invention which activates are also called sequences.
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                 composition comprising an
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Disclosure; Page 1241; 1343pp; English.

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Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating

cancers and respiratory obstructions -Disclosure, Page 763-764; 1592pp; English.

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Human low adenosine antisense oligonucleotide related sequence #2527.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human, airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; hronchodilator; antiinfammation; surfactant depletion; respiratory; hypotensive; cytostatio; immunosuppressive, antiasthmatic; analgesic; hypotensive; cytostation; surfactant hypoproduction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; cancer; ss.

Homo sapiens.

WO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-USO8020.

06-APR-1999; 99US-0127958.

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

Nyce JW;
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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a "Universal" or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with a cativity of target polypeptides associated with a cativity and antibodies, antibody receptors, cytokines and activity of target polypeptides associated with a chemokines, endogenously produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, inding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, defensins, growth factors, vasociated proteins. The receptors, binding proteins and malliquancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (specially pulmonary obstruction and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, allergic rhinitis (AR), pulmonary distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary infections, bronchitis, and/or cancer. AARIB434 to AARIB434 represent human polynucleotide in and/or cancer. Arribation, pulmonary infections, bronchitis, and/or cancer. Arribation rejection, pulmonary infections, bronchitis, and/or cancer. Arribation rejection, pulmonary infections, bronchitis, and/or cancer. Arribation rejection, pulmonary infections of tragments and antisense oligonucleotides used in the exemplification of tragments.

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AAF21322

ΒP

14-MAR-2001 (first entry)

Human low adenosine antisense oligonucleotide related sequence #2889

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human, airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

Homo sapiens.

WO200062736-A2

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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a "Universal" or alternative base. (I) can have respiratory, bronchdiator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adhesion molecules and their receptors, central nervous system (CNS) and peripheral nervous and non-nervous system cesptors, defensine, adhesions molecules and non-nervous system receptors, defensine, and peripheral nervous and non-nervous system creeptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders condition sected from pulmonary associated with a disease or condition selected from pulmonary vasconstriction, and/or lung inflammation, allergy (iss) and/or bronchoconstriction) and/or lung inflammation, allergy is pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary transplantation rejection, pulmonary infections, bronchitis, and antisense oligonucleotides used in the exemplification of the present human polynucleotide
                                                                                                                                                                                                                                                                                                      Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
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The present invention describes a new composition comprising an antisense oligonuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, and analysatic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergy; disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
TGTATGTAGGTGCCTGGGGAGTGTGTGGGTCCTTGGCTCTTGGCCTTTCCCCTTGCAG 1745
                                                                                                          TGTACCTCTGATTTCACCCCAGAGTTGGAGTTCTGCTCAAGGAACGTGTGTAATGTGTAC 1625
                                                                                                                                                                                       ttctgtttggagcccatttctgtgagaccctgtatttcaaatttgcagctgaaaggtgct
                                                                                                                                                                          TTCTGTTTGGAGCCCATTTCTGTGAGACCCTGTATTTCAAATTTGCAGCTGAAAGGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                Human adenosine receptor related polynucleotide SEQ ID NO:2527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 692-693; 1343pp; English.
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e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (CoPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs breast down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA33312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences alfer from the previously named sequences. SEQ ID NO:11 to 1680
                                                                                                                                                                                                                                           differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3233 to AAA33992) are specifically claimed Ons from the present invention. N. B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences
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effects afflict the lungs of a subject. They can be used for treating
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The present invention describes a new composition comprising an artisense oligonuclectide (NN) with low adenosine (up to 15%), which targets nuclected cacids involved in bronchoconstriction, allegies, and/or inflammation. The ON can have antiniflammatory, antiallergies, and/or inflammation. The ON can have antiniflammatory, antiallergies, and/or carling airways, including lung disease associated with inflammation.

CC ampaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating effects afflict the lungs of a subject. They can be used for treating effects afflict the lungs of a subject. They can be used for treating cathma, impeded respiratory vasoconstriction, allergies, asthma, impeded respiratory man and cancers such as leukaemias, lymphomas, cathma, impeded respiratory man cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of decoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA33313 to AAA3312 represent the invention, which correspond to SEQ ID NO:1 to 2815, but the sequences of differ from the previously named sequences. SEQ ID NO:1 to 185, but the present invention, who not match up with their corresponding SEQ ID NO: sequences contained by the present invention do not match up with their corresponding SEQ ID NO: sequences
Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allersy; allersy; allersy disease; bronchoconstiction; inhibitor; antiinflammatory; antiallergic, antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
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gactggtggctggggccctggcactggggctctggctgaggctgagacgggggtgggaagg
                                                 CTGGTGTGGATAGAAACCAGGCAGGACAGTAGATCCCTATGGTTGGATCTCAGCTGGAAG
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Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; burnfactun depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgasic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss

Homo sapiens

WO200062736-A2

26-OCT-2000

24-MAR-2000; 2000WO-US08020

06-APR-1999;

EAST CAROLINA. J W. NYCE (UYEC-) UNIV (NYCE/)

Nyce JW;

WPI; 2000-679539/66

for treating Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for tr cancers and respiratory obstructions

Disclosure; Page 761-762; 1592pp; English

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchdiator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down regulate the expression and or activity of target polypeptides associated with activity and activity of target polypeptides associated with activity and antibodies, antibody receptors, cytokines and activity and antibodies, antibody receptors, cytokines and activity produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, cytokines and chemokine receptors, adenosine receptors, bradykinin receptors, contral nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (specially pulmonary obstruction and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoaciated with a disease or condition selected from pulmonary vasoaciated with a disease (CNS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary transplantation rejection, pulmonary inflammation, emplysema, chronic obstructive pulmonary distress syndrome (Ruspertension, emplysema, chronic obstructive pulmonary distress syndrome confragments and antisense oligonucleotides used in the exemplification of the present invention present invention

Sequence 1696 BP; 315 A; 488 C; 529 G; 364 T; 0 other;

5; 180 240 174 300 360 294 420 354 480 414 474 009 114 Gaps CCCACACAGATGAGCAGCTGCTCAGGGCTGAGCAGGGTCCTGGTGGCCGTGGCTACAGC gcagccagggaggtccgtgaagctgtgttgtcctggagtgactgccggggacccagtgtc CGGTTTACCCACCCGCTACCTCACCTCCTACAGGAAGACACAGTCCTAGGAGCTGATAG CCTGGTGTCTGCCTCCTCCCCCTGCCCCCAGGCCTGGGGCCCCCCCAGGGGTCCAGTATGG GCAGCCAGGCAGGTCCGTGAAGCTGTGTTGTCCTGGAGTGACTGCCGGGGACCCAGTGTC CTGGTTTCGGGATGGGGAGCCAAAGCTCCTCCAGGGACCTGACGGCTAGGGCATGA ACTGGTCCTGGCCCAGGCAGACAGCACTGATGAGGGCACCTACATCTGCCAGACCCTGGA DB 21; Length 1696; 11; 18; Indels 86.1%; Score 1549.2; 98.2%; Pred. No. 0; Pred. No. 0; 0; Mismatches Query Match 86.1 Best Local Similarity 98.2 Matches 1621; Conservative 55 175 121 235 181 241 295 355 415 541 301 361 421 481 à 셤 ò g ò 셤 ö g ò g ŏ q ò a ò

1260 1380 1020 1080 1011 1131 1191 1251 1371 1431 1491 1551 1677 1611 711 840 771 831 951 534 AGCCAGCTGGACATACCCTGCCTCCTGGCCGTGCCAGCCCCACTTCCTGCTCAAGTTCCG TTTGCAGTACCGTCCGGCGCAGCATCCAGCCTGGTCCACGGTGGAGCCAGCTGGACTGGA GGAGGTGATCACAGATGCTGTGGCTGGCTTGCCCCATGCTGTACGAGTCAGTGCCCGGGA TGGGACCATACCAAAGGAGATACCAGCATGGGGCCAGCTACACACGCAGCCAGAGGTGGA gectcaggtggacagecetgetectecaaggecetecetecaaceacaceeteggetaet CCTGGGACTGGTGGCTGGGGCCCTGGCACTGGGGCTCTGGCTGAGGCTGAGACGGGTGG GAAGGATGGATCCCCAAAGCCTGGGTTCTTGGCCTCAGTGATTCCAGTGGACAGGCGTCC AGGAGCTCCAAACCTGTAGAGGACCCAGGAGGCCTTCGGCAGATTCCACCTATAATCCTG GTGCTTGTACCTCTGATTTCACCCCAGAGTTGGAGTTCTGCTCAAGGAACGTGTGTAATG cggtttacccacccgctacctcacctcctacaggaagaagacagtcctaggagctgatag CCAGAGGAGGAGTCCATCCACAGGGCCCTGGCCATGCCCACAGGATCCCCTAGGGGCTGC ccagaggaggagtccatccacagggccctggccatgcccacaggatcccctaggggctgc GAACCCACTGGGTGGTGCCAGCACACGCCTGGATGTGAGCTTGCAGAGCATCTTGCG gaacccactg---ggtgccagcacacgcctggatgtgagcttgcagagcatctgcg CCCTGACCCACCCAGGGCCTGCGGGTAGAGTCAGTACCAGGTTACCCCCGAGGCCTGCG cectgaeceaceceagggeetgegggtagagteagtaceaggttaececegaegectgeg TCTTGCTGGTGTGGATAGAAACCAGGCAGGACAGTAGATCCCTATGGTTGGATCTCAGCT gtgcttgtacctctgatttcaccccagagttggagttctgctcaaggaacgtgtgtaatg TGTACATCTGTGTCCATGTGTGACCATGTGTCTGTGAAG - - CAGGGAACATGTATT - CTC CCGCTGTGTTGTCCACGGGGCTGAGTTCTGGAGCCAGTACCGGATTAATGTGACTGAGGT 1312 1552 1012 1072 1132 1321 1252 1381 1441 1372 1432 1492 535 595 1561 475 655 712 841 901 832 892 1021 952 1081 1141 1201 1261 1192 1501 1621 601 199 721 781 196 g ò g ŏ g ŏ 셤 ò g οχ g à g δy d ò g ò g ò g δ g à Db δ 엄 ò QQ ŏ g á g ŏ g δy g

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1678 IGCATGCATGTATGTAGGTGCCTGGGGAGTGTGTGTGGGTCCTTGGCTCTTGGCCTTTCC 1737
             1738 CCTTGCAGGGTTGTGCAGGTGTGAATAAA 1767
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Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; busined depletuh; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; crespiratory obstruction; pulmonary obstruction; impeded respiration; selfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; Human low adenosine antisense oligonucleotide related sequence #2886 (first entry) 14-MAR-2001 cancer; ss.

24-MAR-2000; 2000WO-US08020 99US-0127958 WO200062736-A2 36-APR-1999; Homo sapiens 26-OCT-2000 

(UYEC-) UNIV EAST CAROLINA. Nyce JW;

WPI; 2000-679539/66

Low adenosine (A) content antisense oligonuclectides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -Disclosure; Page 1324; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antisathmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and mallighanoises, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, cytokine and chemokine receptors, adenosine receptors, bandyknin receptors, central nervous system (CK) and peripheral nervous and non-nervous system (CK) and peripheral nervous and non-nervous system ceceptors, defensins, growth factors, vasocitated proteins. The receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders considered proteins and malignancy associated proteins.

TTTGCAGTACCGTCCGGCGCAGCATCCAGCCTGGTCCACGGTGGAGCCAGCTGGACTGGA 960 

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AGCCAGCTGGACATACCCTGCCTCCTGGCCGTGCCAGCCCCACTTCCTGCTCAAGTTCCG 772 agccagctggacataccctgcctcctggccgtgccagccccacttcctgctcaagttccg

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and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
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                                                                                                                                                                                        Sequence 1696 BP; 315 A; 488 C; 529 G; 364 T; 0 other;
                                                                                                                                                                                                                                        DB 21;
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Matches 1621; Conservative
                                                                                                                                                         the present invention.
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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating of sthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of decoxyadenosine which activates adenosine receptors causing bronked and inflammation. AAA35311 to AAA35312 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID No:11 to 1680 (AAA3233 to AAA3392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CCCAÇAGATGAGCAGCAGCTGCTCAGGGCTGAGCAGGGTCCTGGTGGCCGTGGCTACAGC 180
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syndrome; pain; cystic fibrosis; emphysema; on; chronic obstructive pulmonary disease; COPD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 1696;
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                                     cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
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respiratory distress
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   aggagoticcaaacctgtagaggacccaggagggotticggcagattccacctataaticig 1371
                                                      ggaagttctgtttggagcccatttctgtgagaccctgtatttcaaatttgcagctgaaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                             GGAAGTTCTGTTTGGAGCCCATTTCTGTGAGACCCTGTATTTCAAATTTGCAGCTGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
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antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired alrways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, fibrosis, pulmonary hypertension, memphysema, chronic obstructive pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the relaction and inflammation. AAA33313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present in the sequences listing from the present also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:1 to 1680 (AAA3323 to AAA3323) are specifically claimed ONs from the present invention. N.B. Sequences Sequences SEQ ID NO: sequences invention and another previously named sequences. SEQ ID NO: sequences given in the sequence of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing. 

T; 0 other; Sequence 1696 BP; 315 A; 488 C; 529 G; 364

5; 240 300 360 420 480 540 900 999 720 121 CCCACAGATGAGCAGCAGCTGCTCAGGGCTGAGGCAGGGTCCTGGTGGCCGTGGCTACAGC 180 115 cetggtgtetgeeteeteecectgeececaggeetggggeececaggggtecagtatgg 174 234 294 354 414 474 534 594 654 Gaps gcagccagggaggtccgtgaagctgtgttgtcctggagtgactgccgggggacccagtgtc CGGTTTACCCACCCCCTACCTCCCTACAGGAAGACAGTCCTAGGAGCTGATAG CCTGGTGTCTGCCTCCTCCCCCTGCCCCCAGGCCTGGGGCCCCCCCAGGGGTCCAGTATGG GCAGCCAGGCAGGTCCGTGAAGCTGTGTTGTCCTGGAGTGACTGCCGGGGACCCAGTGTC CTGGTTTCGGGATGGGGAGCCAAAGCTGCTCCAGGGACCTGACTCTGGGCTAGGGCCATGA ACTGGTCCTGGCCCAGGCAGACAGCACTGATGAGGGCACCTACATCTGCCAGACCCTGGA cggtttacccacccgctacctcacctcctacaggaagaagacagtcctaggagctgatag CCAGAGGAGGAGTCCATCCACAGGGCCCTGGCCCATGCCCACAGGATCCCCTAGGGGCTGC CCGCTGTGTTGTCCACGGGGCTGAGTTCTGGAGCCAGTACCGGATTAATGTGACTGAGGT ccgctgtgttgtccacgggggctgagttctggagccagtaccggattaatgtgactgaggt GAACCCACTGGGTGGTGCCAGCACGCCTGCATGTGAGCTTGCAGAGCATCTTGCG DB 21; Length 1696; Indels 18; Query Match

86.1%; Score 1549.2;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 181 241 175 301 361 295 421 355 415 541 475 535 595 481 601 661 721 8 g ò g ò g ð g ŏ g q 셤 ò g à à ò ò

1260 1320 1380 1440 1500 1620 1020 1011 1140 1071 1200 1131 1191 1251 1311 1371 1431 1560 1491 1551 1677 1737 1668 960 891 951 771 900 831 1678 TGCATGCATGTAGTAGGTGCCTGGGGAGTGTGTGTGGGTCCTTGGCCTCTTGGCCTTTCC GGAGGTGATCACAGATGCTGTGGCTGGCCTGCCCCATGCTGTACGAGTCAGTGCCCGGGA CTTTCTAGATGCTGGCACCTGGAGCACCTGGAGCCCGGGGGGGCCTGGGGAACTCCGAGCAC 952 ctttctagatgctggcacctggagcacctggagcccggaggcctggggaactccgagcac 1072 gecteaggtggacageeetgeteetecaaggeeeteeetecaaceacaceteggetact CCTGGGACTGGTGGGCCCCTGGCCACTGGGGCTCTGGCTGAGGCTGAGACGGGGTGG GAAGGATGGATCCCCAAAGCCTGGGTTCTTGGCCTCAGTGATTCCAGTGGACAGGCGTCC 1441 TCTTGCTGGTGTGGATAGAAACCAGGCAGGACAGTAGATCCCTATGGTTGGATCTCAGCT 1372 tettgetggtgtggatagaaaccaggcaggacagtagatccctatggttggatetcaget GGAAGTTCTGTTTGGAGCCCATTTCTGTGAGACCCTGTATTTCAAATTTGCAGCTGAAAG GTGCTTGTACCTCTGATTTCACCCCAGAGTTGGAGTTCTGCTCAAGGAACGTGTGTAATG 1621 TGTACATCTGTGTCCATGTGTGACCATGTGTGTGTAAG--CAGGGAACATGTATT-CTC 1552 tgtacatctgtgtccatgtgtgaccatgtgtctgtgaaggccagggaacatgtattcctc CCCTGACCCACCCAGGGCCTGCGGGTAGAGTCAGTACCAGGTTACCCCCGAGGCCTGCG AGCCAGCTGGACATACCCTGCCTCCTGGCCGTGCCAGCCCCCACTTCCTGCTCAAGTTCCG TTTGCAGTACCGTCCGGCGCAGCATCCAGCCTGGTCCACGGTGGAGCCAGCTGGACTGGA 1738 CCTTGCAGGGTTGTGCAGGTGTGAATAAA 1767 1612 ( 841 901 1201 1261 1321 1561 1669 712 892 1021 1081 1141 1192 1501 781 196 a g a qq 셤 a a a g g q g Db οg В g Q ò Óλ ōλ ŏ à δ QΥ ŏ δ Qγ δy Qγ Q δ Qγ

standard; DNA; 1705 AAT17868 AAT17868 ID AAT1 XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA clone (AAT17868), designated Nr1, codes for the murine interleukin-11 (IL-11) receptor alpha chain (AAR17868). It was isolated from adult mouse liver cDNA libraries cloned in lambda gt10 and ZAP by screening with probes (AAT17870-72) based on a conserved motif (AAR22812) of haemopoietin receptors. The sequence can be inserted into a vector and used for prodn. of IL-11 receptor,
                                                          Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding haemopoietin receptor containing conserved amino acid motif esp. IL-11 receptor alpha chain - used for developing IL-11 (ant)agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for developing therapeutic (ant)agonists or in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.2%; Score 976.4; DB 17; Length 1705; 76.6%; Pred. No. 7e-244; Live 0; Mismatches 366; Indels 34;
                                         Murine interleukin-11 receptor alpha chain DNA clone Nr1
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complement (133..156)
                                                                                                                Location/Qualifiers
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/note= "primer 449"
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                                                                                                                                                                                                                                                                                                                         (AMRA-) AMRAD OPERATIONS PTY LTD.
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Matches 1310; Conservative
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P-PSDB; AAR92813.
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AAT17868,
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         1586 AGAGTTGGAGTTCTGCTCAAGGAACGTGTGTAATGTGTACATCTGTGTCCATGTGTGACC 1645
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Search completed: October 3, 2001, 18:55:32 Job time: 2726 sec

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October 3, 2001, 15:17:45; Search time 1394.56 Seconds (without alignments) 12201.079 Million cell updates/sec
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Copyright (c) 1993 · 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 897)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Unj.W.B., Gruber,C., Jessee,J. and Colayes,D.

Unpublished (2001)

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL562475 897 bp mRNA EST 16-FEB-2001
AL562475 LTI_NFL003_NBC3 Homo sapiens cDNA clone CSODC011YP14
                             Description
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AV593468
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/lab_host="neuroblastoma cells"
/lab_host="neuroblastoma cells"
/note="organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
3 others
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Pred. No. 8.6e-208;
1; Mismatches 6; Indels 2;
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Matches 882; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 846)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                      1628
                                                                                                              1688
                                                                     CCTGGTGTCTGCCTCCTCCCCCTGCCCCCAGGCCTGGGGCCCCCCAGGGGTCCAGTATGG 240
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AL525319 LTI_NPL003_NBC3 Homo sapiens CDNA clone CSODC011YP14
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                                                       ACCTCTGATTTCACCCCAGAGTTGGAGTTCTGCTCAAGGAACGTGTGTAATGTGTACATC
                                                                                                              1629 TGTGTCCATGTGACCATGTGTCTGTGAAGCAGGGAACATGTATTCTCTGCATGT
                                                                                                                           : www.genoscope.cns.fr.
TGTTTGGAGCCCATTTCTGTGAGACCCTGTATTTCAAATTTGCAGCTGAAAGGTGCTTGT
                           231 TGTTTGGAGCCCATTTCTGTGAGACCCTGTATTTCAAATTTGCAGCTGAAAGGTGCTTGT
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                                                                                                                                                                                   2 others
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/lab_host="DH10B"
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BP 191 91006 EVRX cedex - France
Emall: segref@qenoscope.cns.fr, Web : www
Location/Qualifiers
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Pred. No. 2.6e-182;
2; Mismatches 6;
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AL525319
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Matches 784; Conservative
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Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Nathonal institutes of Health, Mammalian Gene Collection (MGC)

Lopublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: gapbs-femalinih, gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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164 Homo sapiens cDNA clone IMAGE:4183J38
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        24.1
        GCAGCCAGGCAGGTCCGTGAAGCTGTGTTGTCCTGGAGTGACTGCCGGGGACCCAGTGTC
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        17.2
        GCAGCCAGGCAGGTCCGTGAAGCTGTGTTGTCCTGGAGTGACTGCCGGGGACCCAGTGTC
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                                                                                                 CTGGTTTCGGGATGGGGAGCCAAAGCTGCTCCAGGGACCTGACTCTGGGCTAGGGCATGA
                                                                                                                          ACTGGTCCTGGCCCAGGCAGCAGCACTGATGAGGGCACCTACATCTGCCAGACCCTGGA
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                                                       // Organism="Homo sapiens"
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/dlone="lyAGE:4183138"
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/tissue_type="dlioblastom with EGFR amplification"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Site_2: Sall; cloned unidirectionally. Primer: Oligo dT. Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                             12; Indels
                                                                                                                                                                                                                                  Query Match 38.2%; Score 687.8; DB 147
Best Local Similarity 98.1%; Pred. No. 1.6e-164;
Matches 717; Conservative 0; Mismatches 12;
            column: 11
http://image.llnl.gov
Plate: LLAW9498 row: o column:
High quality sequence stop: 761.
Location/Qualifiers
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/tissue_type="T_cells from T_cell leukemia"
/tissue_type="T_cells from T_cell leukemia"
/note="Vector: pcMvSPORT 6; Site_1: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched. double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email: filang@lifetech.com URL:
http://fullength.invitrogen.com"

11 a 233 c 170 g 142 t 16 others
                                                                                                                                                                                                                     Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 722)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
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ALDBU490 722 bp mRNA EST 16-FEB-2001 ALSB0490 LTL_NFL008_TC2 Homo sapiens CDNA clone CSODJ015YH07 2000 ALSB0490
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/clone_lib="LTI_NFL008_TC2"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-blo.llnl.gov/Dbrp/Aimage/Aimage.html
Insert Length: 1402 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 457.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 662)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1372 CAGGCGTCCAGGAGCTCCAAACCTGTAGAGGACCCAGGAGGGCTTCGGCAGATTCCACCT 1431 ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
//lab_host="Organ: lung; Vector: pT/T3D-Pac (Pharmacia) with
modified polylinker; lst strand cDNA was prepared from
                                                                                                                                                                                             TITCAAATTTGCAGCTGAAAGGTGCTTGTACCTCTGATTTCACCCCAGAGTTGGAGTTCT 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI857919 662 bp mRNA EST 21-DEC-1999 wj68b07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2407957 similar to TR:Q16542 Q16542 INTERLEUKIN-11 RECEPTOR. ; mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary
                                                               ATAATCCTGTCTTGCTGTGTG------GATAGAAACCAGGCAGGACAGTAGAT
                                                                                                                               CCCTATGGTTGGATCTCAGCTGGAAGTTCTGTTTGGAGCCCCATTTCTGTGAGACCCTGTA
                                                                                                                                                242 CCCTATGGTTGGATCTCAGCTGGAAGTTCTGTTTGGAGCCCATTTCTGTGAGACCCTGTA
                                                                                                                                                                                                                                                                                                                         62 CAGGGAACATGTATTCANTGCATGCATGTATGTAGGTGCCTGGGGAGTGTGTGTGTGGGCCC
                  182 TITCAAAITIGCAGCIGAAAGGGCCITGIACCICCIGAITICACCCCCAGAGIIGGAGIICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NCI_CGAP_Lu19"
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/db_xref="taxon:9606"
/clone="IMAGE:2407957"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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AI857919
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COMMENT

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pooled lung tumor tissue, and was then primed with a Not — oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and Metaima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                             272
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                                                                                                                                                                                        Length
                                                                                                                       others
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Pred. No. 7e-151;
); Mismatches 10; Indels
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210 c 20
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98.0%;
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AW189494
AW189494.1
EST.
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Sequencing Center information can be
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Unpublished (1997)

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can by
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
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/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: uterus, Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                AW438628 611 bp mRNA EST 14-FEB-2000 xt01c12.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2777878 3' similar to TR:Q16542 Q16542 INTERLEUKIN-11 RECEPTOR. ;, mRNA
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                      1697 GCCTGGGGAGTGTGTGGGTCCTTGGCTCTTGGCCTTTCCCCTTGCAGGGGTTGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2777878"
/clone_lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade,
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                                                                                                                                  100 GCCTGGGGAGTGTGTGTGTGGGTCCTTGGCCTTTTCCCCTTGCAGGGTTGTGCAG
                                             611 CCTGGGGTTATTGATCACAGGGACTCTGTGGAGCAGGAAGCTGTGCTGGCGTCTTTGGAA
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                                                                                                                                                                                                                       40 GTGTGAATAAAGAAATAAGGAAGTTTTTGAAAAAAAA 2
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AW438628.1 GI:6973934
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                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #:
                                         Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE: 2675539"
/clone_lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, pooled tumors"
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Pred. No. 2.5e-142;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                            www-bio.llni.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 414.
Location/Qualifiers
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Best Local Similarity 96.2%;
Matches 615; Conservative
                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 640)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 568)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF435972 568 bp mRNA EST 30-MAR-2001 nab/5h05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3738925 3' similar to TR:Q16542 Q16542 INTERLEUKIN-11 BF435972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: capabs.refmail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality: sequence stop: 439.
Location/Qualifiers
                                                                                                                                                                                                   1488
                                                                                                                                                                                                                                                                                              TGCAGCTGAAAGGTGCTTGTACCTCTGATTTCACCCCAGAGTTGGAGTTCTGCTCAAGGA 1608
GAGACGGGGTGGGAAGGATGGATCCCCAAAGCCTGGGTTCTTGGCCTCAGTGATTCCAGT 1368
                                                                                                GGACAGGCGTCCAGGAGCTCCAAACCTGTAGAGGACCCAGGAGGCCTTCGGCAGATTCCA 1428
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                                                                                                                          252 TGCAGCTGAAAGGTGCTTGTACCTCTGATTTCACCCCAGAGTTGGAGTTCTGCTCAAGGA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3273825"
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AUTHORS
TITLE
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a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clonelDS: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NBHSF pool 1: 145032-147325, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NBJERB-9W pool 1: 788280-760583, 772104-774407 Soares NBHRA pool 1: 304776-306311, 320136-322823, 326280-32665 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 563.2; DB 148; Length 568; Pred. No. 8.4e-133; 0; Mismatches 3; Indels 0;
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ilarity 99.5%;
Conservative 0
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/note="Organism in mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                            A1264000 559 bp mRNA EST 27-JAN-1999 qi05b01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1855561 3. similar to TR:Q14626 Q14626 INCOMPLETE INTERLEUKIN-11 RECEPTOR A1264000
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 559) NCI-CGAP http://www.ncbi.nlm.nih;gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_NhHWPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoéimage.llnl.gov) for further information.
Insert Length: 620 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 441.
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                                              481 TCCATCCACAGGGCCCTGGCCATGCCCACAGGATCCCCTAGGGGCTGCCCGCTGTGTTGT
                       613 TCCATCCACAGGGCCCTGGCCATGCCCACAGGATCCCCTAGGGGCTGCCCGCTGTGTTGT
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Pred. No. 6.9e-127;
0; Mismatches 5;
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/clone="IMAGE:1855561"
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                                                       Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was
                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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100.0%; Pred. No. 1.1e-128;
iive 0; Mismatches 0;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                   Seq primer: -400P from Gibco
High quality sequence stop: 494.
Location/Qualifiers
  (bases 1 to 547)
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Best Local Similarity 100.
Matches 547; Conservative
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christe Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL, send email to:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 514)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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CAGGCAGGTCCGTGAAGCTGTGTTGTCCTGGAGTGACTGCCGGGGACCCAGTGTCCTGGT 191
                        TACCCACCCGCTACCTCACCTCCTACAGGAAGACAGTCCTAGGAGCTGATAGCCAGA
                                                                                                                                                                                                                                                   TCCTGGCCCAGGCAGACAGCACTGATGAGGGCACCTACATCTGCCAGACCCTGGATGGTG
                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMMGE:3644593"
/clone=lib="NCI_CGAP_Ov18"
/issue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
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High quality sequence stop: 341.
Location/Qualifiers
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BF434707.1 GI:11446995
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 503)
1 (bases I to 503)
1 (bases I to 503)
2 (bases I, c., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schallenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, Y., Waterston, R. and Wilson, R.
Washu-Merck EST Project 1997
Contact: Wilson RR
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was constructed bento Soares and M. Fatina Bonaldo. " 16c 152 g 97 t 6 others
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Pred. No. 6.9e-116;
0; Mismatches 13; I
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Score 492.6; DB 16; Length
Pred. No. 8e-115;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                   AI149448
AI149448.1 GI:3677917
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Best Local Similarity 99.2%;
Matches 495; Conservative
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RESULT 13
AI149448/C
LOCUS
DEFINITION
                                                                                                                                                                      ORGANISM
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                                                                                                                                                                                                                                                               /lab_host="DH108"
//lab_host="DH108"
//note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI: Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHW, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
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                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:811920"
/clone="IMAGE:811920"
/clone="tayage:"Pooled human melanocyte, fetal heart, and pregnant uterus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 502;
                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL
IMAGE Consortium (info@image.llnl.gov) for further
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
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99.0%; Pred. No. 3.1e-115;
ive 0; Mismatches 5;
                                                                                                                                                 /organism="Homo sapiens"/db_xref="GDB:6042831"
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Best Local Similarity 99.0
Matches 496; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 499)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
AI149448 499 bp mRNA ec72h11.x1 Soares_placenta_8to9weeks_2NbHPBto9W Homo sapiens cDNA clone IMAGE:1715205 3' similar to TR:Q64385 Q64385 INTERLEUKIN 11 ECECTOR, ALPHA CHAIN 2 PRECURSOR; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1724 Std Error: 0.00
Seq primer: -40ml3 fwd. Err from Amersham
High quality, sequence stop: 459.
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Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
sequence: S'-GACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGCAGGCGCCATTATGGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGCAGGCGCATG-GT(30)BN-3' (where B = A,
C, G, OR T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MC Library."
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                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1067)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1507 row: p column: 21
High quality sequence stop: 590.
Location/Qualifiers
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                                                                                 GGTCCTTGGCTCTTGGCCTTTCCCCTTGCAGGGGTTGTGCAGGTGTGAATAAAGAGAATA 11714
 GTTCTGCTCAAGGAACGTGTGTAATGTGTACATCTGTGTCCATGTGTGACCATGTGTCTG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                               clone IMAGE:4690436
                                         31;
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Pred. No. 1.5e-113;
0; Mismatches 115; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phage-resistant)"
                                                                                                                                                                                                                                    BG537915 1067 bp mRNA E 602565788F1 NIH_MGC_77 Homo sapiens cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:4690436"
/clone_llb="NIH_MGC_77"
/lab_host="DH10B (T1 pha
                                                                                                                                                                                                                                                             mRNA sequence.
BG537915
BG537915.1 GI:13530147
                                                                                                                                      1775 AGGAAGTTCTTGGAGATTA 1793
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83.7%;
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302 C
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KEYWORDS
SOURCE
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Homo sapiens
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steploc,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zx99g01.rl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811920 similar to TR:G999450 G999450 INCOMPLETE INTERLEUKIN-11 RECEPTOR ISOEORM ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTACACACGCAGCCAGAGGTGGAGCCTCAGGTGGACAGCCCTGCTGCTCCTAAGGCCCTCC 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGTACGAGTCAGTGCCCGGGACTTTCTAGATGCTGGCACCTGGAGCACCTGGAGCCCG 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTCAGTGATTCCAGTGGACAGGCGTCCAGGAGCTCCAAACCTGTAGAGGACCCAGGAG 1411
                                                                                         CCGGATTAATGTGACTGAGGTGAACCCACTG---GGTGCCAGCACGACGCCTGCTGCTT111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 TGGCGATCTTGGCAAAATCTTTCTTTCCTGGGACTTGGTGGGTTGTGGCCCTGGACTGGG 702
61 ACAGGATCCCCTAGGGGCTG-CCGCTGTGTTGTCCACGGGGCTGAGTTCTGGAGCCAGTA 119
                                                                                                                                                                                                                       CCCACTTCCTGCTCAAGTTCCGTTTGCAGTACCGTCCGGCGCAGC-ATCCAGCCTGGTCC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGGTGGAGCCAGCTGGACGAGGAGGTGATCACAGATGCTGTGGCTGGGCTGCCCCAT 997
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                                                               CCGGATTAATGTGACTGAGGTGAACCCACTGGGTGGTGCCAGCACACGCCTGCTGGATGT
                                                                                                                                                                                         GAGCTTGCAGAGCATCTTGCGCCCTGACCCCACCCCAGGGCCTGCGGGTAGAGTCA-GTAC
                                                                                                                                                                                                                                                                                                                       CAGGTTACCCCCGAGGCCTGCGAGCCAGCTGGACATACCCTGCCTCGTGCCGTGCCAGC
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AA456272.1 GI:2179482
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plaamid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-34549, and 484488-489479."
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                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1810
Finall: est@wastl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. Seq primer: -28m13 rev2 Er from Amersham
High quality sequence stop: 504.
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                    Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.4%; Score 474.4; DB 7; Length 528; 99.0%; Pred. No. 3.6e-110; ive 0; Mismatches 1; Indels 4;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb\_rol:\* gb\_ro2:\* gb\_in4:\* gb\_pr10:\* em\_ba3:\*

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SUMMARIES	ID	BC003110	HSIL11RM	HSU32324	HSIL11RR	AF347936	MMU14412	MMETL	MMIL11
	DB	91	93	97	93	94	94	94	94
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ф	Query Match	91.3	91.0	86.1	63.9	54.6	54.2	54.0	53.9
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AX010400 Sequence AX450283 Homo sapi AL162231 Human DNA G26821 human STS U32323 Human inter C29858 human sTS S X94162 M.musculus X94159 M.musculus X94159 M.musculus X94159 M.musculus X94161 M.musculus X94163 M.musculus X94161 M.musculus X94161 M.musculus X94163 M.musculus X94161 M.musculus X94181 Sequence E28089 Novel IL-6 AR147881 Sus scrof X85298 Human mRNA A93714 Sequence 1 EQ4633 CDNA encodi EC2673 CDNA encodi EC2673 CDNA encodi EC2673 CDNA encodi EC2673 CDNA encodi EC2674 DNA encodi A98693 Sequence 5 X51976 Mouse mRNA X51975 Mouse mRNA X51975 Mouse mRNA X51975 Mouse mRNA X51975 Mouse mRNA X51976 Mouse mRNA X51976 Mouse mRNA X51976 Mouse mRNA X61978 Mus muscu AC073703 Mus muscu AC073703 Mus muscu	
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LENEGGEGESPRPGFLASVIPVDRRFGAPNL"
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Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lilsa Prabhu, Parvaneh Saeedi, Jacquellne Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra
                                                                                                                               Clone distribution: MGC clone distribution information can be fo through the I.M.A.G.B. Consortium/LinL at: http://image.llnl.gov Series: IRAL plate: 6 Row: D Column: 8.
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         CCCTGACCCACCCCAGGGCCTGCGGGTAGAGTCAGTACCAGGTTACCCCCGAGGCCTGCG
                                                                                                                     AGCCAGCTGGACATACCCTGCCTCCTGGCCGTGCCACCTTCCTGCTCAGTTCCG
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/vccduct="interleukin-11 receptor"
/product="interleukin-11 receptor"
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/db_x
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Direct Submission
Submitted (13-OCT-1994) Michel Cherel, Institut de biologie, INSERM
U 211, 9 Quai de Moncousu, Nantes, 44035, FRANCE
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1682)
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/clone_lib="PCDNA I LIBRARY"
/codon_start=1
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/isolate="INDIVIDUAL"
/db_xref="taxon:9606"
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/translation="MSSSCSGLSRVLVAVATALVSASSPCPQAMGPPGVQYGQPGRSV
KLCCPGVTAGDPVSMPRDGERKLLQEPDSGLGHELVLAQADSTDEGTYICQTLDGALG
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RSPSTGPWPCPQDPFGAARCVVHQAEFWSQYRINVTEVNPLGASTRLLDVSLQSILRP
DPPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLLKFRLQYRPAQHPAWSTVEPAGL
EEVITDAAAGLPHAVRVSARDFLDAGTWSTWSPEAWCTPSTGTIPKEIPAWGLHTQP
ELSTTDAAAGLPHAVRVSARDFLDAGTWSTWSPEAWCTPSTGTIPKEIPAWGLHTQP
LRRGGKDGSPRPGFLASVIPVDRRPGAPNL"

1691. .1696
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CTCCAAACCIGTAGAGGACCCAGGAGGCTTCGCCAGATTCCACCTATAATCCTGTCTTG 1445
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1696)
Van Leuven, F., Stas, L., Hilliker, C., Miyake, Y., Billinski, P.
                                                                                                                                                                                            CTGGTGTGGATAGAAACCAGGCAGGACAGTAGATCCCTATGGTTGGATCTCAGCTGGAAG
                                                                               TTCTGTTTGGAGCCCATTTCTGTGAGACCCTGTATTTCAAATTTGCAGCTGAAAGGTGCT
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Submitted (26-JUL-1995) Human Genetics, K.U.Leuven,
Gasthuisberg ON06, Leuven, Belgium, B-3000
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/map="9p13"
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/protein_id="AAB36492.1"
/db_xref="G1:975337"
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/organism="Homo sapi
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Submitted (04-NOV-
U 211, 9 Quai de,
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                                          Indels
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Pred. No. 0;
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J (04-NOV-1994) Michel Cherel, Institut de Biologie, INSERM
Quai de, Moncousu, Nantes, 44035, FRANCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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H.sapiens mRNA for interleukin 11 receptor isoform (incomplete).
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/db_xref="taxon:9606"
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/product="incomplete interleukin-11 receptor isoform"
/product="incomplete interleukin-11 receptor isoform"
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/db_xref="SPTERMBL:016542"
/db_xref="SPTERMBL:016542"
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CCPGVTAGOPYSWRRAGPERVLAGPSCPGTERLLVSRYRKTVLGADSGRES
VTCLGYPARPVVSCQAADYENESCTWSPGJSGLPTRILTSYRKKTVLGADSGRES
PSTGPWPCPQDPLGAARCVVHGAEFWSQYRINVTEVNPLGASTRLLDVSLGSILRPDP
PGGLRVSCYPCPRRILRASMTYPASMPCQPHFLLKFRLQYRRAGPHPAMSTVEPAGLEE
VITDANAGLPHANRVSARDFLDAGTWSTWSPEAMGTPSTGTIPKEIPAMGQLHTQPEV
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                                                                                                                                                                                                                                      63.9%; Score 1149.4; DB 93; Length 1199; 99.7%; Pred. No. 6.5e-286; 1.ve 0; Mismatches 1; Indels 3;
           /tissue_type="placenta"
/clone_lib="PCDM8"
/dev_stage="embryo'
                                                        /codon_start=1
                                                                                                                                                                                                                                                   Best Local Similaring Matches 1163; Conservative
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/product="interleukin 11 receptor alpha chain precursor"
/protein_id="aak29624.1"
/brotein_id="aak29624.1"
/db_xref="di:13549075"
/db_xre
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Li,R., Hartley,L. and Robb,L.
Expression of interleukin-11 and interleukin-11 receptor chain in the rat uterus in the peri-implantation period unpublished
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Robb, L. and Li, R.

Direct Submission
Submitted (08-EEB-2001) Cancer and Haematology Division, and Eliza Hall Institute of Medical Research, PO Royal Me Hospital, Vic 3050, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Eukaryota; Metazoa
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                                                          DB 94; Length 1713;
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                                                          54.6%; Score 982.6; DB 94; llarity 77.9%; Pred. No. 6.9e-243; Conservative 0; Mismatches 334;
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Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Criurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1681)
Hilton, D. J., Hilton, A. A., Raicevic, Å., Rakar, S., Harrison-Smith, M. Godph, N.M., Beglegy, C. G., Metcalf, D., Nicola, N.A. and Willson, T. A. Cloning of a murine IL-11 receptor alpha-chain; requirement for gpl30 for high affinity binding and signal transduction
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Mus musculus interleukin-11 receptor alpha-chain mRNA, complete
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                                              1132 ATCACAGGACCCCTTGGAGCAAGTGGCTGTGTTAGCATCTCTGGGAATCTTCTTTCC
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Pred. No. 5e-241;
0; Mismatches 361; Indels
Submircted (U/-SEP-1994) Douglas J. B
Hall Institute of Medical Research,
                                                                  /organism="Mus musculus"
/strain="C57/B16 x CBA"
/db_xref="taxon:10090"
                            Victoria 3050, Australia
Location/Qualifiers
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MMETL 1719 bp mRNA ROD 17-FEB-1995	do yo	186 CTGGCAGGCCCGTGATGCTGTGCTGCCCCGGAGTGAGTGCTGGGACTCCAGTGTCCTGGT 245
	g qa	TTCGGGATGGAGATTCAAGGCTGCTCCAGGGACCTGACTCTGGGTTAGGACACAGACTGG
receptor gene; enhancer-trap-locus-2; interleukin 11 ise.	Qy Dp	366 TCCTGGCCCAGGCAGACACCTGATGAGGGCACCTACATCTGCCAGACCCTGGATGGTG 425 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1710)	Qy	426 CACTTGGGGGCACAGTGACCTGCAGCTGGGCTACCCTCCAGCCCGCCC
Direct Submission Submitted (07-SEP-1993) A. Gossler, Max-Delbrueck-Lab. in der MPG, Carlvon-Linne-Weg 10, 50829 Koeln, FRG	Qy	486 GCCAAGCAGCCGACTATGAGAACTTCTTGCACTTGGAGTCCCAGCCAG
Coases 1 to 1/10) Neuhauses 1 to 1/10) Neuhaut, J.L. and Gossler, A. et12, a novel putative type-1 cytokine receptor expressed during	Qy Dp	546 TACCCACCGGTACCTCACCTCCTACAGGAAGAAGACAGTCCTAGGAGCTGATAGCCAGA 605
	Qy	606 GGAGGAGTCCATCCACAGGCCCTGGCCATGCCCAGGATCCCCTAGGGGTGCCCGCT 665
Direct Submission Submitted (17-FEB-1995) A. Gossler, The Jackson Laboratory, 600 Main Street, Bar Harbour, MEO 04609, USA	Qy Dp	666 GTGTTGTCCACGGGGCTGAGTTCTGGAGCCAGTACCGGATTAATGTGACTGAGGTGAACC 725 
on reb 20, 1999 This sequence Version replaced gl:003/10. Location/Qualifiers 1. 1719 //crganism=Mus musculus"	Qy Dp	726 CACTGGGTGGTGCCAGCACGCCTGCTGGATGTGAGCTTGCAGGATCTTGCGCCCTG 785
or, o	Qy	786 ACCCACCCCAGGGCCTGCGGGTAGAGTCAGTACCAGTTACCCCCGAGGCCTGCGAGCCA 845 1
/gene="Et12/IL11 rec" 681366 /gene="Et12/IL11 rec"	Qy	846 GCTGGACATACCCTGCCTGCCGTGCCACCTCCACTTCCTGCTCAAGTTCCGTTTGC 905
/product="cytokine type 1 receptor" /protein_id="cAA52908.1" /db_xref="d1:67498" /db_xref="wch.wcr.1001?"	QQ Oy	906 AGTACCGTCCGGCGCAGCATCCAGCTGGTCCACGGGGGGGG
/db_xref="spTREMBL:109123" /db_xref="SPTREMBL:064385" /translation="MSSSCSGLTRVLVAVATALVSSSSPCPQAWGPPGVQYGQPGRPV /translation="MSSSCSGLTRVLVAVATALVSSSSPCPQAWGPPGVQYCQTLGOVSG /translation="mss"	Qy	966 TGATCACAGATGCTGTGGCTGGGCTGCCCATGCTGTACGAGTCAGTGCCCGGGACTTTC 1025   1111   1111111111111111111111111111
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LEARNSGROGEOGREES SUCCESSION TO THE SECOND OF THE SECOND O	Qy	1086 CCATACCAAAGGAGATACCACCATGGGGCCAGCTACCACGCAGCCAGAGGTGG 1139 11
54.0%; Score 972; DB 94; Length 1719; Carity 77.3%; Pred. No. 3.8e-240; Concerty 140	Qy	1140 AGCCTCAGGTGGACAGCCCTGCTCCAAGGCCCTCCCTCCAACCACCACCTCGGCTAC 1199
AGGGCTGAGCAGGTCCTGGTGGCCGTGGCTACAGCCCTGG 185	Qy	1200 TTGATCACAGGGACTCTGTGGAGCAGGTGCTGCTGGCGCCTTTGGGAATCCTTTCTT 1259 
3CAGC 24	Oy Db	1260 TCCTGGGACTGGTGGCTGGGGCCCTGGCACTGGGCTCTGGCTGAGGCTGAGACGGGGTG 1319
CTGGT 30		1320 GGAAGGATGGATCCCCAAAGCCTGGGTTCTTGGCCTCAGTGATTCCAGTGGACAGGCGTC 1379

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/db_xref="MGD:MGI:109123"
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/db_xref="SPTREMBL:P70225"
/translation="MSSSCGGTRVLYARTALVSSSSPCPQAMGPPGVQYGQPGRPV
MLCCPGVSAGTPVSRFRDGDSFLLQEPDSGLHRLVLAQVDSPDEGTYVCQTLDGVSG
GMVTLKLGFPPARPEVSCQAVDYENFSCTWSPGQVSGLPTRYLTSYRKKTLPGAESQR
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Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases 1 to 1985)
Bilinski,P., Hall,M.A., Neuhaus,H., Gissel,C., Heath,J.K. and
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                                                                                                                                                                                                                                                   ATGTGTACA----GAAGTCTGTGTTTCCTGTGATCGTGTGTGTATGTGAGACAGGGAGCA 1612
                                                                                                                                                                                                                                                                                                                                                                                 Two differentially expressed interleukin-11 receptor genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCCTTTCCCCTTGCAGGGGTTGTGCAGGTGTGAATAAAGAGAATAAGGAAGTTCTTG 1786
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                     1323 CAGGAATTCCAAACCTGCAGAGGACCCCAGAGAACTTCAGCTGATTTCATCTGTAACCCG
                                                                         GTCTTGCTGGTGGATAGA------AACCAGGCAGGACAGTAGATCCCTATGGT
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11 receptor.
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house mouse.
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Submitted (17-JUN-1996) A. Gossler, The
Main Street, Bar Harbor, ME 04609, USA
Related sequences: X94157-X94163.
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/protein_id="CAA67144.1"
/db_xref="G1:1654014"
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/tissue_type="testis"
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314. 1612
/gene="IL-11 receptor"
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1. .1985
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SOURCE
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ESPSTGPWPCPQDPLEASRCVVHGAEFWSEYRINVTEVNSLGASTCLLDVRLQSILRP
DPPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLLKFRLQYRPAQHPAWSTVEPIGL
EEVITOTVAGLEHAVRVSARDFLDAGTWSAWSPEAWGTPSTGILQDEIPDWSGGHGQQ
LEAVVAQEDSLAPARPSLQPDPRPLDHRDFLEQVAVLASLGIFSCLGLAVGALALGLW
LRLRRSGKEGPQRGLLAPMIPVEKLGIPNLQRTPENFS"

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                                                                                                      Length 1985;
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                                                                                                      94;
                                                                                                                             338;
                                                                                                     53.9%; Score 970.2; DB 94 llarity 77.4%; Pred. No. 1.1e-239; Conservative 0; Mismatches 338;
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Matches 1308;
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ESPSTGPWPCPQDPLEASRCVVHGAEFWSEYRINVTEVNSLGASTCLLDVRLQSILRP
DPPQGLRVESVPGXPRRQPHFLKRRLQYRAGATRQPHFLKRELQY
EEVITDTVAGLPHAVRYSARDFLDAGTWSAWSPEAMGTPSTGLLQDEIPDWSGGHGQQ
LEAVVAQEDSLAPARPSLQPDRFPLDHRDPLEQVAVLASLGIFSCLGLAVGALGLM
LRLRRSGKEGPQKPGLLAPMIPVEKLPGIPNLQRTPENFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSSSCSGLTRVLVAVATALVSSSSPCPQAMGPPGVQYGQPGRPV
MLCCPGVSAGTPVSWFRDGDSRLLQGPDSGLGHRLVLAQVDSPDEGTYVCQTLDGVSG
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                                                                                                                                                                      Submitted (05-SEP-1996) Walter and Eliza Hall Institute of Research, Post Office, Royal Melbourne Hospital, Parkville, Victoria 3050, Australia Location/Qualifiers
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Robb.L., Hilton,D.J., Brook-Carter,P.T. and Begley,C.G.
Rothification of a second murine interleukin-11 receptor
alpha-chain gene (ILI)Ra2) with a restricted pattern of ex
Genomics 40 (3), 387-394 (1997)
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/protein_id="AAC53114.1"
/db_xref="GI:1916004"
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   (23), 13754-13761 (1996)
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                                                                                                                                                                                                                                                                                                                                 cDNA library"
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/organism="Mus musculus"
/strain="CD-1"
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/clone_lib="CD-1 cDNA
302. .1600
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                                                                                                                                                                                                                                                                                                    /chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                           /gene="IL11Ra2"
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Structural analysis of the gene encoding the murine interleukin-11
receptor alpha-chain and a related locus
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Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1975)
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chain (IL11Ra2) mRNA,
TCTAGATGCTGCCACCTGGAGCACCTGGAGCCCGGAGGCCTGGGGAACTCCGAGCACTGG
                 1740 AACTIGCIGCCGGCTGAAGGCTGTGTGCTTCTGATGTCCTGAGGTGGAAGTCCACCTG
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                                                                              ACTIGATCACAGGGACTCTGTGGAGCAGGTAGCTGTGCTGGCGTCTTTGGGAATCCTTTC
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                                                              GACCATACCAAAGGAGATACCAGCATGGGGCCAGCTACACACGCAGC-----CAGAGGT
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IL11 receptor alpha
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TTTACCCACCGGTACCTCACTCCTACAGGAAGAAGACAGTCCTAGGAGCTGATAGCCA 	GAGGAGGACTCCATCCACAGGCCCTGGCCATGCCCACAGGATCCCTAGGGGCTGCCG	CTGTGTTGTCCACGGGGCTGAGTTCTGGAGCCAGTACCGGATTAATGTGACTGAGGTGAA 	CCCACTGGGTGGTGCCAGCACACGCCTGGATGTGAGCTTGCAGAGCATCTTGCGCCC	TGACCCACCCCAGGGCCTGCGGGTAGAGTCAGTACCAGGTTACCCCCGAGGCCTGCGAGC	CAGGTGGACATACCCTGCCTCCTGGCCGTGCCAGCCCCACTTCCTGCTCAGTTCCGTTTTTTTT	GCAGTACCGTCCGGCGCAGCATCCAGCCTGGTCCACGGTGGAGCCAGCTGGACTGGAGGAGA   11	GGTGATCACAGATGCTGTGGCTGGCTGCCCCATGCTGTACGAGTCAGTGCCGGGACTT 	TCTAGATGCTGGCACCTGGAGCACCTGGAGGCCTGGGGAACTCCGAGCACTGG	GACCATACCAAAGGAGATACCAGCATGGGGCCAGCTACACACGCAGCCAGAGGT 	GGAGCCTCAGGTGGACAGCCCTGCTCCTCCAAGGCCTCCCTC	ACTIGATCACAGGGACTCTGTGGAGCAGGTAGCTGTGCTGGCGTCTTTGGGAATCCTTTC	TITCTGGGACIGGTGGCTGGGCCCTGGCACTGGGGCTCTGGCTGAGGCTGAGGCGGGGCTGAGGAGCGAG	TGGGAAGGATGGATCCCCAAAGCCTGGGTTCTTGGCCTCAGTGATTCCAGTGGACAGGCG 	TCCAGGAGCTCCAAACCTGTAGAGGACCCAGGAGGCTTCGGCAGATTCCACCTATAATC 	CTGTCTTGCTGGTGTGGATAGAAACCAGGAGGAGGACAGTAGATCCCTATG 	GTTGGATCTCAGCTGGAAGTTCTGTTGGAGCCCATTTCTGTGAGACCCTGTATTTCA 	AATITGCAGCIGAAAGGIGCIIGIACCICIGAITICACCCCAGAGIIGGAGIICIGCICA 
AGTCCTAGGA             GCTGCCAGGA	GATCCCTA          GACCCTCTG	SATTAATGTG 	TTGCAGAGC	TACCCCGA	TTCCTGCTC	GAGCCAGCT	CGAGTCAGT	TGGGGAACT	ACGCAGC            GGACAGCAG	CTCCAACCA             TTGCAGCCA	GCGTCTTTG              GCATCTCTG	TGGCTGAGG	GTGATTCCA	GGCAGATTC 	AGGCAGGACAGTA                AGGCGGGCAGTG	TTTCTGTGAGAC              TTTCTTTGACA-	CAGAGTTGGA             CTGAGGTGGA
GAAGAAGACI               GAAGAAGACC	ATGCCCACAC              GTGTCCACAC	CCAGTACCGC          TGAGTACCGC	GGATGTGAGG               GGATGTGAGA	AGTACCAGG1 	CCAGCCCCAC 	GTCCACGGTC 	CCATGCTGTA            CCACGCGGTA	CCCGGAGGCC                CCCAGAGGCC	GACCATACCAAAGGAGATACCAGCATGGGGCCAGCTACACACGCAGC 	AAGGCCCTCC 	AGCTGTGCTC	ACTGGGGCTC 	CTTGGCCTC2	GGAGGCCTTCG         AGAGAACTTCA	AACCAGO	GAGCCCATT1              GAGCTCTTT1	GATTTCACCC     TTCTGATGTC
CTCCTACAG	GCCCTGGCC             GCCTTGGCC	GTTCTGGAG	ACGCCTGCT	GGTAGAGTC	CTGGCCGTG         CTGGCGTCG	TCCAGCCTG	resecrece 	CACCTGGAG            CGCCTGGAG	AGCATGGGG         TGATTGGAG	recreeres            Gereeres	GGAGCAGGT 	GGCCCTGGC	GCCTGGGTT 	GAGGACCCA              GAGGACCCC	A       AAGGACAGG	TTCTGTTTG	TGTACCTCT      TGTCTGGAC
SCTACCTCAC	ATCCACAGG	CGGGGCTGA        TGGGGCAGA	TGCCAGCAC 	AGGCCTGCG	ACCCTGCCTC	GGCGCAGCA 	vrgcrgrggc          vracrgrgg	CACCTGGAG 	GGAGATACC            TGAGATACC	GGACAGCCC	GGACTCTGT	GGTGGCTGG	ATCCCCAAA 	TCCAAACCTGTAGAGGACCC. 	CTGTCTTGCTGGTGGATAGA 	GTTGGATCTCAGCTGGAAGTTC 	AAAGGTGCT 
ACCCACCG 	SAGGAGTCC   	TGTTGTCCA 	ACTGGGTGC        ACTGGG	CCCACCCCA	CTGGACATA 	STACCGTCC             %TACCGACC	GATCACAGA 	AGATGCTGG	CATACCAAA 	SCCTCAGGI        \GCTCAGGA	rgatcacag 	CCTGGGACT	SAAGGATGG 	TCCAGGAGCTCC            CCAGGAATTCC	TCTTGCTGG	SGATCTC           GAGGTCTC	TTGCAGCTG
544	604	664	724	784 955	844	904	964	1024	1084	1138	1198	1258	1318	1378	1438	1487 1675	1545
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Mmmmalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
1 (bases 1 to 1140)
Austin, R.C. and Shaughnessy, S.
Osteoporosis treatment
Patent: WO 9959608-A 3 25-NOV-1999;
HAMILTON CIVIC HOSPITAL RESEAR (CA)
1. 0.1140
/organism="Murinae gen. sp."
//db.xref="taxon:39108"
ator
223 a 344 c 347 g 226 t
                   1725 TCTTGGCCTTTCCCCTTGCAGGGTTGTGCAGGTGAATAAAGAGAATAAGGAAGTTCT 1784
                                                                                                                                           1605 AGGAACGTGTGTAATGTGTACATCTGTGTCCATGTGTGACCATGTGTCTGTGAAGCAGGG 1664
                                                            180
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                                                                            248 GGCAGGTCCGTGAAGCTGTGTTGTCCTGGAGTGACTGCCGGGGACCCAGTGTCCTGGTTT
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83.0%; Pred. No. 1.7e-191;
tive 0; Mismatches 179; Indels 9;
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                                                                                                                                                                                                                                                                                                   AX010400 1140 bp DNA
Sequence 3 from Patent W09959608.
AX010400 GI:9997251
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Murinae gen. sp.
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31609 CCAAGATCCGGTCTTACTGTCTCTCCTGATTTGCCTCCTGCTTCTTCTAGGAGCTCCAAA 31668
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                                          Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 175329 bases at least Q40
Consensus quality: 175422 bases at least Q30
Consensus quality: 175505 bases at least Q20
Insert size: 175642; sum-of-contigs
Insert size: 125620; 6.2% error; agarose-fp
Ouality coverage: 12.58x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1513 TGGAGCCCATTTCTGTGAGACCCTGTATTTCAAATTTGCAGCTGAAAGGTGCTTGTACCT
                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGTAGAGGACCCAGGAGGCCTTCGGCAGATTCCACCTATAATCCTGTCTTGCTGGTGT
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Pred. No. 1.9e-98;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment:01129.0"
19743. 139602
/note="assembly_fragment:01129.1"
139703. 176042
                                                                                                                                                                                                                                                                          coverage: 14.57x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment:02019
fragment_chain:1"
7925. .12446
/note="assembly_fragment:00438
fragment_chain:1"
12547. .19642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment:02616"
a 41038 c 43488 g 46696 t
    Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-443P11"
/clone_lib="RPCI-11.2"
                         name: bA443P11
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93.8%;
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Best Local Similarity 93.8
Matches 439; Conservative
                         Center project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1088 ATACCAAAGGAGATACCAGCATGGGGCCAGCTACACACGCAGC-----CAGAGGTGGAG 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      968 ATCACAGATGCTGTGGCTGGGCTGCCCCATGCTGTACGAGTCAGTGCCCGGGACTTTCTA 1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908 TACCGTCCGGCGCAGCATCCAGCCTGGTCCACGGTGGAGCCAGCTGGACTGGAGGAGGTG
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  CCCACCCGCTACCTCACCTCCTACAGGAAGAAGACAGTCCTAGGAGCTGATAGCCAGAGG
                                                                                                                                                                                                                                                                                                                                                                CCACCCCAGGGCCTGCGGGTAGAGTCAGTACCAGGTTACCCCCGAGGCCTGCGAGCCAGC
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                                                                                         AGGAGTCCATCCACAGGGCCCTGGCCATGCCCACAGGATCCCCTAGGGGCTGCCGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA HTG Clone RP11-443P11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 9 clone R
PROGRESS ***, 5 unordered pieces.
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                             /note="Sequence from overlapping clone bA443P11 (AL450283). Assembly confirmed by restriction digest
                                                                                                                                                                                                             /note="Sequence from AC026658 sequenced by WUGSC." 40220 c 43034 g 53483 t
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STS; STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
                                                                                                                                 /note="Single clone region. Assembly confirmed by restriction digest data." 181125. .181171
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                            DB 90;
                                                                                                                                                                                                                                                                                                                                       Score 421.6; DB 90;
Pred. No. 1.9e-98;
0; Mismatches 29;
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Mammalia, Eutheria, Primates,
1 (bases 1 to 411)
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human STS STS_Z38102,
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93.8%;
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19; Conservative
                                                                                 data.'
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Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, Callo 15A, UK. E-mail enquiries: humquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

On Feb 27, 2001 this sequence version replaced gi:12956907.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone: and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; WP:, NORMBEP; Information on the WORMPEP than their source databases: Em:, EMBL; Sw:, Alternation of the WORMPEP.
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Human DNA sequence from clone RPI1-195F19 on chromosome 9, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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31789 TGGAGCCCATTTCTGTGAGACCCTGTATTTCAAATTTGCAGCTGAAAGGTGCTTGTACCT 31848
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RP11-195F19 is from the library RPCI-11.1 constructed by the of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACG3.6
This sequence is the entire insert of clone RP11-195F19 The tright end of clone RP11-43P11 is at 124461 in this sequence.
                                                   AGGTGCCTGGGGAGTGTGTGTGTGGGTCCTTGGCTCTTGGCCTTTCCCCTTGCAGGGGTTGT
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/db_xref="taxon:9606"
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/clone="RP11-195F19"
/clone_lib="RPCI-11.1"
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sednence. AL162231

ACCESSION

VERSION

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AL162231

human.

ORGANISM

KEYWORDS

Clark, G.

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

Euteleostom1;

source

FEATURES

02-JUN-1996

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join(2073. .2172,2463. .2523,3597. .3766,3893. .4007,
4161. .4193,4279. .4445,5376. .5539,6595. .6736,7110. .7229,
7340. .7436,7690. .7772,8319. .8335)
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KLCCPGVTAGDPVSWFRDGEPKLLQGPDSGLGHELVLAQADSTDEGTYICQTLDGALG
GTVTLQLGYPPARPVVSCQAADYENFSCTWSPSQISGLPTRYLTSYRKKTVLGADSQR
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PDPGLHVESSYPGYPRRLEASMYTYBARDCPHELLKRRLQYRAQYRPAGHPAGE
EEVITDAAGLPHARVSARDFLDAGTWSFWSPERWGTSTGTIPKELPAWGCHTQP
EVEPQVDSPAPPRPSLQPHPRLLDHRDSVEQVAVLASLGILSFLGLVAGALALGLWLR
                                                                                                                                                                                                                                                                                                                 Gossler,A. Molecular cloning and characterization of the human interleukin-11 receptor alpha-chain gene, IL11RA, located on chromosome 9p13 Genomics 31 (1), 65-70 (1996) 96404003
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9286)
                                                                                                                                                                                                                                                                                      Van Leuven, F., Stas, L., Hilliker, C., Miyake, Y., Bilinski, P. and
  HSU32333 9286 bp DNA PRI 22-NOV-1996
Human interleukin-11 receptor alpha chain gene, complete cds.
U323233
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Submitted (26-JUL-1995) Human Genetics, K.U.Leuven, Campus
Gasthuisberg ONO6, Leuven, Belgium, B-3000
Location/Qualifiers
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/protein_id="AAB36491.1"
/db_xref="G1:975335"
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2463. .2523
/number=3
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/db_xref="taxon:9606"
/map="9p13"
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/number=6
4279. .4445
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/number=10
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8696. .8701
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/number=4
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/number=12
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/db_xref="taxon:9606"
/map="166.4 cR from top of Chr9 linkage group"
70. .288
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul
                                                                         Primer A: GCAGGACAGTAGATCCCTATGG
Primer B: GCATGCAGAGAATACATGTTCC
STS size: 219
PCR Profile:
                        Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67. .288)
118 g
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                                                                                                                                                                                                         Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
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1 76 c 118
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Primer: each 5 pM
dNTPs: each 4 nM
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KC1: 50 mM
Tris-HCL: 10 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.4
Best Local Similarity 98.8
Matches, 399; Conservative
Fax: 617 252 1902
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                                                                                                                                                                                                                       1512
                                                                                            8269 CCAAGATCCGGTCTTACTGTCTCTCTCTGTTTGCCTCCTGCTTCTTCTAGGAGCTCCAAA 8328
                                                                                                                                                                  8329 CCTGTAGAGGACCCAGGAGGCTTCGGCAGATTCCACCTATAATTCTGTCTTGCTGGTGT 8388
                                                                                                                                                                                                                                                                                           1513 TGGAGCCCATTTCTGTGAGACCCTGTATTTCAAATTTGCAGCTGAAAGGTGCTTGTACCT 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGATTTCACCCCAGAGTTGGAGTTCTGCTCAAGGAACGTGTGTAATGTGTACATCTGTG 1632
                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCATGTGTGACCATGTGTGTGTGAAG -- CAGGGAACATGTATT-CTCTGCATGCATGTA 1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1690 TGTAGGTGCCTGGGGAGTGTGTGGGTCCTTGGCTCTTGGCCTTTCCCCTTGCAGGGT 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-0CT-1996
                                                                                                                                                                                                                                          1333 CCCAAAGCCTGGGTTCTTGGCCTCAGTGATTCCAGTGGACAGGCGTCCAGGAGCTCCAAA
                                                                                                                                                                                                                     1453 GGATAGAAACCAGGCAGGACAGTAGATCCCTATGGTTGGATCTCAGCTGGAAGTTCTGTT
                                                                                                                                               1393 CCTGTAGAGGACCCAGGAGGCTTCGGCAGATTCCACCTATAATCCTGTCTTGCTGGTGT
   Length 9286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305,
Teat: 4157259687
Frax: 4157259689
Email: myers@shgc.stanford.edu
Score 338.8; DB 97; Length
Pred. No. 7.7e-77;
0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STS; STS sequence; primer; sequence tagged site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1750 TGTGCAGGTGTGAATAAAGAAATAAGGAAGTTCTTGGAGAT 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA STS sequence tagged site.
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Primer B: GCATGCAGAGAATACATGTTCC
STS size: 219
PCR profile:
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Polymerization:
PCR Cycles:
Thermal Cycler:
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human STS SHGC-35540,
G29858
   18.8%;
89.2%;
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Query Match 18.8
Best Local Similarity 89.2
Matches 412; Conservative
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ACCESSION
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COMMENT
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-- Washington University/Merck EST sequence.
Location/Qualiflers
1. 219
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. 219
1. 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1586 AGAGTTGGAGTTCTGCTCAAGGAACGTGTGTAATGTGTACATCTGTGTCCATGTGTGACC 1645
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                                                                                                                                                                                                                                                                                                                                                                                            54; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 215.8; DB 5
Pred. No. 8.5e-45;
0; Mismatches 2
               each 1 um
each 200 um
0.05 units/ul
10 ul
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                                                                                                     2.5 mM
50 mM
20 mM
8.3
                                                                                                                                                                                                                                                                                                                    .219)
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                                          Taq Polymerase:
Total Vol:
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Best Local Similarity 99.1%;
Matches 217; Conservative 0
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Tris-HCl:
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                 Primer:
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                                                                                      Buffer:
                                                                                                                                                                                                                                                                                                  primer_bind
primer_bind
count
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